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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/462,846

DATE: 02/02/2001
TIME: 16:35:53

Input Set : A:\GC381-US-seqlist.txt
Output Set: N:\CRF3\02022001\I462846.raw

3 <110> APPLICANT: Estell, David A.
5 <120> TITLE OF INVENTION: Proteases From Gram-Positive Organisms
8 <130> FILE REFERENCE: GC381-US
10 <140> CURRENT APPLICATION NUMBER: US 09/462,846
11 <141> CURRENT FILING DATE: 2000-01-13
13 <150> PRIOR APPLICATION NUMBER: PCT/US98/19529
14 <151> PRIOR FILING DATE: 1998-07-14
16 <150> PRIOR APPLICATION NUMBER: EP 97305227.7
17 <151> PRIOR FILING DATE: 1997-07-15
19 <160> NUMBER OF SEQ ID NOS: 7
21 <170> SOFTWARE: FastSEQ for Windows Version 3.0
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24 <211> LENGTH: 945
25 <212> TYPE: DNA
26 <213> ORGANISM: Bacillus subtilis
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31 gccgcgcata aaaaatggta aagcgttggtt caaaaacggaa tggataaggg gttcacgctc 180
32 agcgaattat gggaaacatca caacattttt ttcggacagc ttgaaggggg ccgtttccct 240
33 ctgcttacaa aaatattttaga tgctgaccag gacttatactg ttcaggtgca tccgaatgtat 300
34 gaatatgcca acatacatga aaacygtgag cttygaaaaa cagaatgtg gtacattatt 360
35 gattgccaaa aagatgccc gattttat ggcacaaatgg caacaacaaa ggaagaacta 420
36 actaccatga tagagcgtgg agaatggat gagctttgc gccgtgtaaa ggtaaagccg 480
37 ggggattttt tctatgtgcc aagcggtaact gttcatgcqaa ttggaaaaagg aattcttgc 540
38 ttggagacgc agcagaactc agacacaacc tacagattat atgattatga ccgaaaagat 600
39 gcagaaggca agctgcgcga gcttcatctg aaaaagagca ttgaagtgtat agaggccc 660
40 tctattcccg aacggcatac agttcacccat gacaaatggg aggtttgtc tacaacgcaca 720
41 ttgattgaat ggcgttactt ttcgtgggg aaatggact ttcaggatc agcaagctta 780
42 aagcagccaa aaccattctc tcttatactgt gtgattgaag gggagggccg tttgtatctct 840
43 ggtgatgtatg tctatccctt caaaaaagga gatcatatgt tgctgcctta cggctttgg 900
44 gaatttaaac tcgaaggata tgccaaatgt atcgtctccc atctg 945
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47 <211> LENGTH: 315
48 <212> TYPE: PRT
49 <213> ORGANISM: Bacillus subtilis
51 <400> SEQUENCE: 2
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54 Trp Gly Gly Thr Ala Leu Ala Asp Phe Phe Gly Tyr Thr Ile Pro Ser Gln
55 20 25 30
56 Arg Thr Gly Glu Cys Trp Ala Phe Ala Ala His Gln Asn Gly Gln Ser
57 35 40 45
58 Val Val Gln Asn Gly Met Tyr Lys Gly Phe Thr Leu Ser Glu Leu Trp
59 50 55 60
60 Glu His His Arg His Leu Phe Gly Gln Leu Glu Gly Asp Arg Phe Pro
61 65 70 75 80

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62 Leu Leu Thr Lys Ile Leu Asp Ala Asp Gln Asp Leu Ser Val Gln Val
63 85 90 95
64 His Pro Asn Asp Glu Tyr Ala Asn Ile His Glu Asn Gly Glu Leu Gly
65 100 105 110
66 Lys Thr Glu Cys Trp Tyr Ile Ile Asp Cys Gln Lys Asp Ala Glu Ile
67 115 120 125
68 Ile Tyr Gly His Asn Ala Thr Thr Lys Glu Glu Leu Thr Thr Met Ile
69 130 135 140
70 Glu Arg Gly Glu Trp Asp Glu Leu Leu Arg Arg Val Lys Val Lys Pro
71 145 150 155 160
72 Gly Asp Phe Phe Tyr Val Pro Ser Gly Thr Val His Ala Ile Gly Lys
73 165 170 175
74 Gly Ile Leu Ala Leu Glu Thr Gln Gln Asn Ser Asp Thr Thr Tyr Arg
75 180 185 190
76 Leu Tyr Asp Tyr Asp Arg Lys Asp Ala Glu Gly Lys Leu Arg Glu Leu
77 195 200 205
78 His Leu Lys Lys Ser Ile Glu Val Ile Glu Val Pro Ser Ile Pro Glu
79 210 215 220
80 Arg His Thr Val His His Glu Gln Ile Glu Asp Leu Leu Thr Thr Thr
81 225 230 235 240
82 Leu Ile Glu Cys Ala Tyr Phe Ser Val Gly Lys Trp Asn Leu Ser Gly
83 245 250 255
84 Ser Ala Ser Leu Lys Gln Gln Lys Pro Phe Leu Leu Ile Ser Val Ile
85 260 265 270
86 Glu Gly Glu Gly Arg Met Ile Ser Gly Glu Tyr Val Tyr Pro Phe Lys
87 275 280 285
88 Lys Gly Asp His Met Leu Leu Pro Tyr Gly Leu Gly Glu Phe Lys Leu
89 290 295 300
90 Glu Gly Tyr Ala Glu Cys Ile Val Ser His Leu
91 305 310 315
93 <210> SEQ ID NO: 3
94 <211> LENGTH: 220
95 <212> TYPE: PRT
96 <213> ORGANISM: *Bacillus subtilis*
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100 1 5 10 15
101 Gln Lys Gly Ala Val Thr Pro Val Lys Asn Gln Gly Ser Cys Gly Ser
102 20 25 30
103 Cys Trp Ala Phe Ser Ala Val Val Thr Ile Glu Gly Ile Ile Lys Ile
104 35 40 45
105 Arg Thr Gly Asn Leu Asn Glu Tyr Ser Glu Gln Glu Leu Leu Asp Cys
106 50 55 60
107 Asp Arg Arg Ser Tyr Gly Cys Asn Gly Gly Tyr Pro Trp Ser Ala Leu
108 65 70 75 80
109 Glu Leu Val Ala Gln Tyr Gly Ile His Tyr Arg Asn Thr Tyr Pro Tyr
110 85 90 95
111 Glu Gly Val Gln Arg Tyr Cys Arg Ser Arg Glu Lys Gly Pro Tyr Ala
112 100 105 110

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113 Ala Lys Thr Asp Gly Val Arg Gln Val Gln Pro Tyr Asn Glu Gly Ala
114 115 120 125
115 Leu Leu Tyr Ser Ile Ala Asn Gln Pro Val Ser Val Val Leu Glu Ala
116 130 135 140
117 Ala Gly Lys Asp Phe Gln Leu Tyr Arg Gly Gly Ile Phe Val Gly Pro
118 145 150 155 160
119 Cys Gly Asn Lys Val Asp His Ala Val Ala Ala Val Gly Tyr Gly Pro
120 165 170 175
121 Asn Tyr Ile Leu Ile Lys Asn Ser Trp Gly Thr Gly Trp Gly Glu Asn
122 180 185 190
123 Gly Tyr Ile Arg Ile Lys Arg Gly Thr Gly Asn Ser Tyr Gly Val Cys
124 195 200 205
125 Gly Leu Tyr Thr Ser Ser Phe Tyr Pro Val Lys Asn
126 210 215 220
128 <210> SEQ ID NO: 4
129 <211> LENGTH: 948
130 <212> TYPE: DNA
131 <213> ORGANISM: *Bacillus subtilis*
133 <400> SEQUENCE: 4
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135 gttttaegag atagattttg atacagtatt ctttcagaat caacggggga atgtctggcc 120
136 atttccgcctc atccaaaagg accgagactt gttgcaatg gcccgataaa aggaaajaca 180
137 ttgatcgagc tttggaaaga gcacccgtgaa gtattccggcg qcgttagaggg ggatcggtt 240
138 ccgcttctga caaagctgtt ggatgtgaag gaagatacgt caattaaagt tcaccctgtat 300
139 gattactatg ccggagaaaa cgaagggga gaactccggca agacggaaatg ctggtaacatt 360
140 atcgaactgta aggaaaacccg agaaatcatt tacggccata cggcccyctt aaaaaccgaa 420
141 ctgtcacaat tgatcaacag cggtaactgg gagggccctgc tgcaagaat caaaattaa 480
142 ccgggtgtatt tctattatgt gccgagccggaa acgctgcacg cattgtgcac gggggccctt 540
143 gtttttagaga ctcagcaaaa ttcagatgcc acataccggg tttacgatata tgaccgtctt 600
144 gatagcaacg gaagtcccgag agagttcat tttgccaag cggtaatgc cgccacgtt 660
145 ccccatgtgg acggatataat agatgaatcg acagaatcaa gaaaaggat aaccattaa 720
146 acatttgcac aaggggataa ttttcgggtt tataatggg acatcaatgg cgaagctgaa 780
147 atggctcagg atgaatccctt tctgatgtgc acgctgttag aaggaaagccg tttgctcaag 840
148 tatgaggaca aaacatgtcc gctaaaaaaa ggtgatcaat ttatccggc ggctcaatg 900
149 cccgatattt cgtataaagg aacttgtacc ttatcgtgt ctcatatt 948
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152 <211> LENGTH: 316
153 <212> TYPE: PRT
154 <213> ORGANISM: *Bacillus subtilis*
156 <400> SEQUENCE: 5
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159 Trp Gly Gly Thr Ala Leu Arg Asp Arg Phe Gly Tyr Ser Ile Pro Ser
160 20 25 30
161 Glu Ser Thr Gly Glu Cys Trp Ala Ile Ser Ala His Pro Lys Gly Pro
162 35 40 45
163 Ser Thr Val Ala Asn Gly Pro Tyr Lys Gly Lys Thr Leu Ile Glu Leu
164 50 55 60
165 Trp Glu Glu His Arg Glu Val Phe Gly Val Glu Gly Asp Arg Phe

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166 65          70          75          80
167 Pro Leu Leu Thr Lys Leu Leu Asp Val Lys Glu Asp Thr Ser Ile Lys
168          85          90          95
169 Val His Pro Asp Asp Tyr Tyr Ala Gly Glu Asn Glu Glu Gly Glu Leu
170          100         105         110
171 Gly Lys Thr Glu Cys Trp Tyr Ile Ile Asp Cys Lys Glu Asn Ala Glu
172          115         120         125
173 Ile Ile Tyr Gly His Thr Ala Arg Ser Lys Thr Glu Leu Val Thr Met
174          130         135         140
175 Ile Asn Ser Gly Asp Trp Arg Glu Gly Leu Leu Arg Arg Ile Lys Ile Lys
176          145         150         155         160
177 Pro Gly Asp Phe Tyr Tyr Val Pro Ser Gly Thr Leu His Ala Leu Cys
178          165         170         175
179 Lys Gly Ala Leu Val Leu Glu Thr Gln Gln Asn Ser Asp Ala Thr Tyr
180          180         185         190
181 Arg Val Tyr Asp Tyr Asp Arg Leu Asp Ser Asn Gly Ser Pro Arg Glu
182          195         200         205
183 Leu His Phe Ala Lys Ala Val Asn Ala Ala Thr Val Pro His Val Asp
184          210         215         220
185 Gly Tyr Ile Asp Glu Ser Thr Glu Ser Arg Lys Gly Ile Thr Ile Lys
186          225         230         235         240
187 Thr Phe Val Gln Gly Glu Tyr Phe Ser Val Tyr Lys Trp Asp Ile Asn
188          245         250         255
189 Gly Glu Ala Glu Met Ala Gln Asp Glu Ser Phe Leu Ile Cys Ser Val
190          260         265         270
191 Ile Glu Gly Ser Gly Leu Leu Lys Tyr Glu Asp Lys Thr Cys Pro Leu
192          275         280         285
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195 Ile Lys Gly Thr Cys Thr Leu Ile Val Ser His Ile
196          305         310         315
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199 <211> LENGTH: 945
200 <212> TYPE: DNA
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203 <400> SEQUENCE: 6
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206 tctgcacatg cccatggctc gtcgtctgta aaaaatggcc cyctggcagg aaagacacctt 180
207 gatcaagatg gaaaagatca tccagagata ttccgggttcc cggatggtaa ggtgtttccg 240
208 ctgctgttaa agctgtggc cgcacatatg gatctctccg tgcacagtccaa tcctqatqat 300
209 gattatgcaa aactgcacga aatggcgac cttggtaaaa cgyagtgtctg gtatatcatt 360
210 gatttgcacaa atgacgcggc actaatttttq ggcacatcatg caagcacaata ggaaggatgc 420
211 aaacaacgaa tagaaagcgg tgatttggaaac gggctgtctg ggcgaatcaa aatcaagcca 480
212 ggagattttc ttatgtgtcc aaggcggtaca ctccatgttt tatgttaaggg aacccttgc 540
213 cttgaatcc agcaaaactc tqataacaata tattcgcgtat acgattatga ccgcgtataat 600
214 gaccaggccc aaaaagaac tttttttata gaaaaagccca tggaaagtcat aacgataccg 660
215 catatcgata aagtgcatac accggaaagta aaaaagttt gtaacgcgtga gatcattttt 720
216 tatgtcaat cagattattt ctcagtgtaa aatggaaaga ttacggccg agctgtttt 780

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217 cttccatatac aaacctatTTT gctggggagt gttctgagcg gatcaggacg aatcataaat 840
 218 aatggtattc agtataatg caatgcaggc tcacacttta ttctgcctgc gcatttttga 900
 219 qaatttacaa tagaaggaac atgtgaattc atgatatctc atct 945
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 222 <211> LENGTH: 315
 223 <212> TYPE: PRT
 224 <213> ORGANISM: *Bacillus subtilis*
 226 <400> SEQUENCE: 7
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 228 1 5 10 15
 229 Gly Gly Thr Lys Leu Arg Asp Ala Phe Gly Tyr Ala Ile Pro Ser Gln
 230 20 25 30
 231 Lys Thr Gly Glu Cys Trp Ala Val Ser Ala His Ala His Gly Ser Ser
 232 35 40 45
 233 Ser Val Lys Asn Gly Pro Leu Ala Gly Lys Thr Leu Asp Gln Val Trp
 234 50 55 60
 235 Lys Asp His Pro Glu Ile Phe Gly Phe Pro Asp Gly Lys Val Phe Pro
 236 65 70 75 80
 237 Leu Leu Val Lys Leu Leu Asp Ala Asn Met Asp Leu Ser Val Gln Val
 238 85 90 95
 239 His Pro Asp Asp Tyr Ala Lys Leu His Glu Asn Gly Asp Leu Gly
 240 100 105 110
 241 Lys Thr Glu Cys Trp Tyr Ile Ile Asp Cys Lys Asp Asp Ala Glu Leu
 242 115 120 125
 243 Ile Leu Gly His Ala Ser Thr Lys Glu Glu Lys Gln Arg Ile
 244 130 135 140
 245 Glu Ser Gly Asp Trp Asn Gly Leu Leu Arg Arg Ile Lys Ile Lys Pro
 246 145 150 155 160
 247 Gly Asp Phe Phe Tyr Val Pro Ser Gly Thr Leu His Ala Leu Cys Lys
 248 165 170 175
 249 Gly Thr Leu Val Leu Glu Ile Gln Gln Asn Ser Asp Thr Thr Tyr Arg
 250 180 185 190
 251 Val Tyr Asp Tyr Asp Arg Cys Asn Asp Gln Gly Gln Lys Arg Thr Leu
 252 195 200 205
 253 His Ile Glu Lys Ala Met Glu Val Ile Thr Ile Pro His Ile Asp Lys
 254 210 215 220
 255 Val His Thr Pro Glu Val Lys Glu Val Gly Asn Ala Glu Ile Ile Val
 256 225 230 235 240
 257 Tyr Val Gln Ser Asp Tyr Phe Ser Val Tyr Lys Trp Lys Ile Ser Gly
 258 245 250 255
 259 Arg Ala Ala Phe Pro Ser Tyr Gln Thr Tyr Leu Leu Gly Ser Val Leu
 260 260 265 270
 261 Ser Gly Ser Gly Arg Ile Ile Asn Asn Gly Ile Gln Tyr Glu Cys Asn
 262 275 280 285
 263 Ala Gly Ser His Phe Ile Leu Pro Ala His Phe Gly Glu Phe Thr Ile
 264 290 295 300
 265 Glu Gly Thr Cys Glu Phe Met Ile Ser His Pro
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